

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: November 9, 2001, 09:54:43 ; Search time 96.37 Seconds

(without alignments)  
10822.295 Million cell updates/sec

Title: US-09-001-737-7

Perfect score: 1661

Sequence: 1 GAATCGCGCTCATATGCA.....TGGCGGATACCGAATTC 1661

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues 1460202

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

N\_Geneseq\_0601.\*  
1: /SIDSI/gcgdata/geneseq/geneseq/NA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
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21: /SIDSI/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1661	100.0	1661	20	AAH86155
2	1052	63.3	1661	20	AAH86155
3	1038.4	62.3	1926	22	AAH86155
4	1033.4	62.3	1926	22	AAH86155
5	942.6	56.7	1926	22	AAH86155
6	704.2	42.4	1647	18	AAH86155
7	704.2	42.4	1647	18	AAH86155
8	654.2	39.4	1647	22	AAH86155
9	590.6	35.5	1647	21	AAH86155
10	589.8	35.5	1647	21	AAH86155
11	589.8	35.5	1647	22	AAH86155

12	589.8	35.5	4524	21	AAA48500	Escherichia coli g
13	568.2	34.2	1662	20	AAH86154	DNA encoding a Str
14	552.8	33.3	1635	21	AAH86154	Neisseria meningit
15	551.6	33.2	910715	20	AAH20248	Borrelia burgdorfe
16	550	33.1	2465	12	AAH01335	Hsp operon. Chlam
17	536.8	32.3	1635	21	AAA13000	Neisseria meningit
18	536.8	32.3	1635	21	AAH25408	Neisseria meningit
19	536.8	32.3	13423	21	AAH81527	N. meningitidis pa
20	536.8	32.3	349980	21	AAH81489	Neisseria meningit
21	528.6	31.8	1838	14	AAH47926	N. meningitidis pa
22	528.6	31.8	1838	14	AAH47926	Hsp60 DNA. Helico
23	528.6	31.8	2223	12	AAH01337	Hsp operon. Chlam
24	528.6	31.7	1724	19	AAH14495	H. pylori GHPRO 118
25	527	31.7	1724	19	AAH14495	H. pylori GHPRO 118
26	526.6	31.7	1635	21	AAH25407	Neisseria gonorrhoe
27	512	30.8	1847	22	AAH32452	Pseudomonas aerugi
28	511.2	30.8	1725	22	AAH32453	Complete genome se
29	505.8	30.5	1038602	20	AAH01425	Helicobacter pylor
30	496.6	29.9	2284	16	AAH01425	Heat shock protein
31	496.6	29.9	2284	16	AAH01425	Heat shock protein
32	496.6	29.9	2322	16	AAH05321	Staphylococcus aur
33	483.2	29.1	3613	9	AAH80339	C. glutamicum SRT
34	470	28.3	1017	18	AAH74577	Nucleotide sequenc
35	464.2	27.9	1737	22	AAH70886	Nucleotide sequenc
36	461.6	27.8	2847	22	AAH25014	Nucleotide sequenc
37	460	27.7	1947	22	AAH25019	Nucleotide sequenc
38	458.6	27.6	1623	22	AAH25002	Nucleotide sequenc
39	458.6	27.6	1920	22	AAH25012	Sequence encoding
40	458.6	27.6	4260	9	AAH81768	Sequence of Mycob
41	458.6	27.6	4380	9	AAH80222	Mycobacterium tube
42	458.6	27.6	4380	19	AAH05708	Nucleotide sequenc
43	448.8	26.9	1656	20	AAH11371	Brevibacterium fla
44	448.8	26.8	1647	17	AAH14265	M. vaccae antigen
45	444.8	26.8	1569	19	AAH34608	

#### ALIGNMENTS

RESULT 1	AAH86155	standard; DNA; 1661 BP.
ID	AAH86155	
XX	AAH86155;	
AC		
XX		
DT	22-SEP-1999 (first entry)	
XX		
DE	DNA encoding a Streptococcus pyogenes heat shock protein (Hsp)60-2.	
XX		
KW	Heat shock protein; Hsp60-2; Immune response; Immunological carrier;	
KW	cancer control; tumour; sarcoma; cancer; gene therapy; ss.	
XX		
OS	Streptococcus pyogenes.	
XX		
PN	WO9935270-A1.	
XX		
PD	15-JUL-1999.	
XX		
PF	29-DEC-1998; 98MO-CA01203.	
XX		
PR	31-DEC-1997; 97US-0001737.	
XX		
PA	(STRE-) STRESSGEN BIOTECHNOLOGIES CORP.	
XX		
PI	Mizzen L, Wisniewski J;	
XX		
DR	WPI: 1999-430397/36.	
XX		
PT	P-PSDB; AAY23904.	
XX		
PT	New nucleic acid encoding heat shock protein-60 from Streptococcus,	
XX	useful in vaccines, as carriers for other immunogens, as anticancer	
XX	agents and for diagnosis	

PS Claim 3; Fig 4A-B; 176bp; English.

XX The present sequence encodes a heat shock protein, designated Hsp60-2.  
 CC The protein, its fragments, variants and fusion proteins, are  
 CC used to elicit or enhance an immune response against Streptococcus,  
 CC and to elicit a similar response to a target antigen fused to the  
 CC protein. Unlike other immunological carriers, Hsp60 proteins are not  
 CC immunosuppressive so provide an increased response to any conjugated or  
 CC fused antigen. Also, where used for cancer control, they lack the side  
 CC effects associated with endotoxins. They can also be used to detect  
 CC specific antibodies and in treatment or prevention of tumours  
 CC (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or  
 CC liver). The Hsp60 polynucleotide is used for recombinant production  
 CC of the protein, as a source of primers and probes for detecting  
 CC streptococci in standard hybridization/amplification assays, and  
 CC therapeutically in gene therapy vectors.

XX Sequence 1661 BP; 512 A; 308 C; 407 G; 434 T; 0 other;

Query Match 100.0%; Score 1661; DB 20; Length 1661;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GAATGGGCTCATATGCGCAAAAGAAATTCATTTCACAGATCCGCTCTCCATGG 60
DB 1 gaatcggctcatatgcaaaagaaatcatttcacagatcgctctccatgg 60
OY 61 TGGCGGAGTTGATATGTTAGCAGATACCGTCAAGTAACGCTTGCTTAAAGGCGCA 120
DB 61 tgcgaggatgatattgttagcagataccgtcaagtaacgcttgctttaaaggcgca 120
OY 121 ATGTGTTCTTGAAAAAGCTTTTGTTCTCCCTTATTAATCAATACGGGTAACCTTG 180
DB 121 atgtgttcttgaaaaagctttgttctcccttatttaataacgggtaaccttg 180
OY 181 CTAAAGAGATCGAATTAGAGATCATTTTGAATAACGTGGAGCAAAATTTGGTGTGAA 240
DB 181 ctaaaagatcgaattagaagatcatttgaataacgtggagcaaaaatttgggtgaa 240
OY 241 TGGCTTCTTAAACCAATGATATGCTGTGATGGAGCGCTCTGCAACGTTTGAAC 300
DB 241 tggcttctttaaaccaatgatattgctgtgatggagcgctctgcaacgtttgaac 300
OY 301 AAGCCATTGTTATGAGAGACTAAAAATGTGACAGCAGGTGCTTATCAATTGGATCC 360
DB 301 aagccattgttatagagactaaaaatgtgacagcaggtgcttataccaattggatcc 360
OY 361 GTGAGGCAATTGAACAGCAACAGACAGCTGTTGAAGCCCTGAAAGCCATTGCTCAAC 420
DB 361 gtgaggcaattgaacagcaacagacagcgttgaagccctgaaagccattgctcaac 420
OY 421 CTGTATCTGCGAAGAGACTTTGCTCAGTGGCTGCGATCATCAAGCTTGAAAG 480
DB 421 ctgtatctgcgaagagactttgctcagtggctgcgatcatcaagcttgaaag 480
OY 481 TTGGAGATATATCTCAGAAAGCTATGAGCGTGTGGGCAAGCATGCTGATTACCATG 540
DB 481 ttggagatatatctcagaaagctatgagcgtgtgggcaagcatgctgattaccatg 540
OY 541 AAGAAATCTGAGGTATGGAAGAACTTGAAGTGTGAAGGATGCAATTTGACCGTG 600
DB 541 aagaaatctgaggtatggaaagaaacttgaagtgtgaaggatgcaatttgaccgtg 600
OY 601 GTTACCTGTCTCAATACATGATGTCACAGACATGAAGAAATGTTGACCTTGAAGAC 660
DB 601 gttacctgtctcaatacatgatgtctcacagacatgaagaaatgttgacacctgaagac 660
OY 661 CATTATCTTATACAGGATAAAAAGTGTCAACAATCAAGATATTTCCACTCTTG 720
DB 661 cattatcttatacaggataaaaagtgtcaacaatcaagatattttccactcttg 720
OY 721 AGGAAGTTCTTAAAAACCAACCGTCAATCAATTAATTGAGATGATGTGATGTGAAG 780

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DB 721 aggaagttcttaaaccaaccgctccatctacatctgcagatgctgagtgag 780
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DB 781 cacttcaacctgtcttgaacaagatgttgatgttcaatgtttctgctcaag 840
OY 841 CGCAGATTTTGATGATGCTGTAAAGCTTGAACATGCTTGAACGTTGACAGTG 900
DB 841 cgcagattttgatgatgctgttaaagcttgaacatgcttgaacgttgacagt 900
OY 901 GTACAGTATTTACAGAGATCTAGACTTGAATTAAGATCTCAATGACACCCCTG 960
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DB 961 gacaggctgctaaagttaacagttgaataagatgacacatattgtgaagtgagaa 1020
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DB 1021 gttacagagcttattgcttaccgtatttgcactgattaatcgcaattgacaaactt 1080
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DB 1141 ttatcaagtatgagagcttcaacagacagctttaaagaaatgaaacttcgctagg 1200
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DB 1201 atgctctaatatgctacacgtgacccggttgaagagtatcgttgctgtgtgaacag 1260
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DB 1261 cacttataccggtatttgaagaaagtacagcttgtgagcttgagggagatgctactg 1320
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DB 1321 gacgtaaatgctctgctgctctgtatgaagacctgtacgtcgaatttgcctttaa 1380
OY 1381 GGTACGAAGGCTCGTATGATTAAGCAAGTTAAAGAGCCCTGACAGAAAGATTTA 1440
DB 1381 ggtacgaaggctcgtatgatattaagcaagtttaagagccctgacagaaagattta 1440
OY 1441 ATGCTGCAACAGGTGAGTGGTGTGATTAATTAACAGCAATATTGACCTGTCAAG 1500
DB 1441 atgctgcaacaggtgagtggtgtgatattaataacagcaatattgacctgtcaag 1500
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DB 1501 taacagatcagcgcttcaaaatgacagcttctgtagacttattttgacaacgagag 1560
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DB 1561 cagtgtgcttaatttaacctggaaacgataccggacccgacgaatccacagcatg 1620
OY 1621 ATCCAGAAATGATGGGTGGATGGCGGATTAAGCCGAATTC 1661
DB 1621 atccagaaatgatgggtggatggcggaatgaagccgaatttc 1661

```

RESULT 2

AA86153 standard; DNA; 1654 BP.

AA86153;

22-SEP-1999 (first entry)

DNA encoding a Streptococcus pneumoniae heat shock protein (Hsp)60-2.

XX Heat shock protein, Hsp60-2; Immune response; Immunological carrier;  
 KW cancer control; tumour; sarcoma; cancer; gene therapy; ss.  
 XX Streptococcus pneumoniae.  
 OS MO9035270-A1.  
 XX PN 15-JUL-1999.  
 XX 29-DEC-1998; 98MO-CA01203.  
 XX PF 31-DEC-1997; 97US-0001737.  
 XX PR (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.  
 XX PA Mlizen L, Wisniewski J;  
 XX PI WPI: 1999-430397/36.  
 XX DR P-PSDB; AAY23902.  
 XX PS New nucleic acid encoding heat shock protein-60 from Streptococcus,  
 PT useful in vaccines, as carriers for other immunogens, as anticancer  
 PT agents and for diagnosis

PS Claim 3; Fig 2A-B; 176pp; English.

CC The present sequence encodes a heat shock protein, designated Hsp60-2.  
 CC The protein, its fragments, variants and fusion proteins, are  
 CC used to elicit or enhance an immune response against Streptococcus,  
 CC and to elicit a similar response to a target antigen fused to the  
 CC protein. Unlike other immunological carriers, Hsp60 proteins are not  
 CC immunosuppressive so provide an increased response to any conjugated or  
 CC fused antigen. Also, where used for cancer control, they lack the side  
 CC effects associated with endotoxins. They can also be used to detect  
 CC specific antibodies and in treatment or prevention of tumours  
 CC (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or  
 CC liver). The Hsp60 polynucleotide is used for recombinant production  
 CC of the protein, as a source of primers and probes for detecting  
 CC streptococci in standard hybridization/amplification assays, and  
 CC therapeutically in gene therapy vectors.

XX Sequence 1654 BP; 500 A; 326 C; 401 G; 427 T; 0 other;

Query Match 53.38; Score 1052; DB 20; Length 1654;  
 Best Local Similarity 77.7%; Pred. No. 1,3e-265;  
 Matches 1771; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

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 DB 1 gaattcggcttcataatgcaaaagaataatttcatacgaatgcccgttcgcataag 60  
 QY 61 TCGCGGAGGTGATATGTATGACGATACCGTCAAGTACCGTGTCTTAAAGGCGCA 120  
 DB 61 tccgcgaggtgatattgtatgacgataccgtcaagtaaccttggagccaaaggttcga 120  
 QY 121 ATGTGTTCTTGAAGAAAGCTTTTGGTTCCTTAAATTAATGAGGAGGATTAACATTG 180  
 DB 121 atgtgttcttgaagaaagcttttggttcccttaattactaatgagggatgacattg 180  
 QY 181 CTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
 DB 181 ctaagagatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 240  
 QY 241 TGGCTTCTAAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
 DB 241 tggcttctaaaccaatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 300  
 QY 301 AAGCCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
 DB 301 aagccatgttgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 360

QY 361 GTGAGGATGTAAGAACAGCAACAGCAACAGCTGTGAAGCCTTGAAGCAATGCTCAAC 420  
 DB 361 gtgaggatgttaagaaacagcaacagcaacagctgtgaagccttgaagcaatgctcaac 420  
 QY 421 CTGTATCTGGCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
 DB 421 ctgtatctggcagagagatgatgatgatgatgatgatgatgatgatgatgatgatgat 480  
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 DB 481 ttgagagtatatctcagaaagctatgagagctgtgagcaaacagatgatgatgatgat 540  
 QY 541 AAGAACTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
 DB 541 aagaaactctgagatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 600  
 QY 601 GTTACCTGTCTCAATACATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 DB 601 gttacctgtctcaatacatgatgatgatgatgatgatgatgatgatgatgatgatgat 660  
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 DB 661 catTTATCTTATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
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 QY 781 CACTTTCACACCTCTGTTTGAACAGATGATGATGATGATGATGATGATGATGATGATG 840  
 DB 781 cacttTCACACCTCTGTTTGAACAGATGATGATGATGATGATGATGATGATGATGATG 840  
 QY 841 CGCGAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
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 DB 1081 ctGACTTGTACCGTGAAGAAAGCTGCAAGAAAGCTGTTGAGGAAATGATGATGATG 1140  
 QY 1141 TTATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
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 QY 1261 CACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320  
 DB 1261 cactTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320  
 QY 1321 GACGTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380  
 DB 1321 gacGTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380  
 QY 1381 GGTACAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440  
 DB 1381 ggtACAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440  
 QY 1441 ATGCTGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1500

Db 1441 acgacgaactgagcagtggtgtaacatgcatgtaacaggtatcatgtaacagtaag 1500  
 Oy 1501 TAACAGCATCAGCGCTTCAAAATGCAGCTTGTAGCTGTCTTATTTTGACACAGAAG 1560  
 Db 1501 tgggtcgctcagccctacaaatcagcagcatctgtgacccctgtgatttgacaacagaag 1560  
 Oy 1561 CAGTTGTGCTTAATTAACCTGAACAGCTAGCCAGCCAGCCCAATGCCAGCAGTATGG 1620  
 Db 1561 cagtcgtagcacaataaacacagacagtagccacagctccagcaatgagatccaaagtatga 1620  
 Oy 1621 ATCCAGCAATGATGGG 1636  
 Db 1621 tgggtgtaagtggcg 1636  
 RESULT 3  
 AAF25036  
 ID AAF25036 standard; DNA; 1926 BP.  
 AC AAF25036;  
 DT 30-APR-2001 (first entry)  
 DE Nucleotide sequence of Hsp65-E7 fusion protein.  
 XX  
 KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;  
 KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;  
 KW E7 protein; ss.  
 XX  
 OS Synthetic.  
 OS Streptococcus pneumoniae.  
 OS Human papillomavirus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1926  
 FT /tag\_2  
 FT /product- "Hsp65-E7 fusion protein"  
 XX  
 PN MO200104344-AZ.  
 PD 18-JAN-2001.  
 PF 10-JUL-2000; 2000OMO-US18828.  
 PR 08-JUL-1999; 99US-0143757.  
 XX  
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.  
 XX  
 PI Siegel M, Chu NR, Mizzzen LA;  
 DR WPI: 2001-138361/14.  
 DR P-PSDB: AMB31619.  
 PT Screening for compounds that stimulate Th1-like responses in CD4+ T  
 PT lymphocyte cells -  
 PS Example 15; Fig 15A-B; 88pp; English.  
 XX  
 CC The present sequence encodes a fusion protein comprising a  
 CC Streptococcus pneumoniae heat shock protein (Hsp) 65 fused to a HPV16 E7  
 CC protein. The fusion protein is used in the method of the invention. The  
 CC specification describes a method of determining whether a compound  
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+  
 CC T lymphocyte cells. The method comprises contacting naive lymphocytes  
 CC in vitro with a fusion protein comprising at least a fragment of Hsp,  
 CC and then detecting the Th1-like response exhibited by the cell sample.  
 CC The proteins which may be used in the method of the invention are Hsp65,  
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify  
 CC compounds that stimulate Th1-like responses in response to microbial  
 CC pathogens.  
 XX  
 SO Sequence 1926 BP; 585 A; 382 C; 464 G; 495 T; 0 other;

Query Match 62.58; Score 1038.4; DB 22; Length 1926;  
 Best Local Similarity 77.55; Pred. No. 5.2e-262;  
 Matches 1238; Conservative 0; Mismatches 366; Indels 0; Gaps 0;  
 Oy 15 ATGGCAAAAGAAATCAATTTTTCAGCAGATGCCCGCTGCTCATGTGCGGAGATTGAT 74  
 Db 1 atggcaaaagaatcaaatatttcacagatgcccgcgtcagctatgctcggtggtgat 60  
 Oy 75 ATGTAGCAGATACCGCTCAAGTACCGCTTGCTTAAAGGCGCATGTGTTCTTGA 134  
 Db 61 atccttcagagatacctgtaagtaacttgggcccacaaagtcgcaatgcttcttgaa 120  
 Oy 135 AAAGCTTTGGTTCCTTCAATTAATGAGCGGGTAAACCATGCTTAAGAGATCGAA 194  
 Db 121 aagcattcggctccaccttgattaccaaagagtggtgactatgcccagaagaattgaa 180  
 Oy 195 TTAGAAGATCAATTTGAAACATGGGAGCAAAATTTGCTGTGAAGTGCTTAAACC 254  
 Db 181 ttagaagacacatttgaataataatggtgcccnaattggtatcagaagtgtctcaaaacc 240  
 Oy 255 AATGATATTGCTGTGATGGAGCAGCTACTGCAACAGTTTTCACACAGCCATTGTCAT 314  
 Db 241 aatgatattgctgtgatggagcagctactgcaaacagttttgacacagccattgtcagt 300  
 Oy 315 GAAGACATAAAATGTGACAGCAGGAGGTAATCAATTTGATTCGCTGAGCATTTGAA 374  
 Db 301 gaagacataaaaatgtgacagcagagtgcaatccaacccggtatcgtcggtgattgaa 360  
 Oy 375 ACAGCAGACGACAGCAGCTGTTGAAGCCTTGAAACCATGCTCAACCTGATTCGCAAG 434  
 Db 361 acagcagtcgagcagagtgatgaaacttggaaaacacagtcacatcccttgccaataaa 420  
 Oy 435 GAAGCTATTGCTCAGTCCGCTCAGATATCATCAGCTGATGAAAGTTGGAGGTATATC 494  
 Db 421 gaagctatcgctcaagttgacgcgcatcttcgttctgtaaaaagtgtgtgtatcacc 480  
 Oy 495 TCAGAAAGCTATGAGCGCTGTGGCAACGATGCTGATTTACCATCGAAGAAATTCGAGGT 554  
 Db 481 tcgaagaagctatgagaaagtgtgcaaaagcgtgtcacacacatcgaagatcagtcgtg 540  
 Oy 555 ATGGAACAGAACTTGAAGTGTGTTGAAGCAGCAATTTGACCGTGTACGTCTCAA 614  
 Db 541 atggaacagagcttgaagtcgtgagaagaatgagcaggttgcgtgtaccccttcacag 600  
 Oy 615 TACATGCTCACAGCAATGAAATGCTTGCAGACCTTGAACCCATTATCTTAATC 674  
 Db 601 tacatgctcacagcaatgaaatgcttgcagaccttgaacccattatctttaatc 660  
 Oy 675 ACGGATAAAAAGTGTCAACATCCAAAGCATTTTGCACCTACTTGAAGAAGTTCTTAA 734  
 Db 661 acggataaaaagtgtcaaacatccaaagcattttgcaccttggaaagcatctccaa 720  
 Oy 735 ACCAAGCGTCATTACTCATTTATTCAGATGATGATGATGATGATGATGATGATGATGAT 794  
 Db 721 agcaatcgctcaactctgattatcgcgagtcgagtcgagtcgagtcgagtcgagtcgagtc 780  
 Oy 795 GTCTTGAACAAGATTCGTGACTTTCATGATGATGATGATGATGATGATGATGATGAT 854  
 Db 781 gtttgaacaagatcttgagaaaccttcacagcagagcagagcagcagcagcagcagcagc 840  
 Oy 855 GATGCTGTTAAGCTATGCTTGAAGCAATTTGATTTGATGATGATGATGATGATGATGAT 914  
 Db 841 gatgctgttaagctatgcttgaagcaatttgatttgaagtgatgagtgatgagtgatgagtgat 900  
 Oy 915 GAGGATTTAGACTTGAATTAAGATGCTACATGACAGCCCTTGACAGCGCTGTAG 974  
 Db 901 gaagacttctgtcttgatgaaagatgcaaaatgagtcgtcttgacgaagagagga 960  
 Oy 975 ATTACAGTTGATTAAGATGACAGATTAATGATGATGATGATGATGATGATGATGATGAT 1034  
 Db 961 gtgacgttgacaaagatgacagcgttatttgaagaagtgacgaagaatccctgaagcatt 1020

[illegible]

XX	MEI: 1998-272225/24.	
XX	Computer-readable medium with recorded Streptococcus pneumoniae	
PT	polynucleotide sequences - useful in diagnostic kits and assays, and	
PT	pharmaceutical compositions and vaccines for Streptococcus	
PT	pneumoniae	
XX		
PS	Claim 1: Page 628-631; 1405pp; English.	
XX		
CC	The present invention describes a computer-readable medium which has	
CC	the nucleotide sequences SEQ ID NO.1 to 391 (AAV52124 to AAV52224)	
CC	recorded on it, or a representative fragment or a sequence at least 95%	
CC	identical to SEQ ID NO. 1 to 391. The nucleotide sequences depicted in	
CC	SEQ ID NO.1 to 391 (AAV52124 to AAV52224) are genomic fragments from	
CC	Streptococcus pneumoniae. The present invention also describes an	
CC	isolated nucleic acid molecule encoding a homologue of any of the	
CC	fragments of the S.pneumoniae genome (SEQ ID NO.1 to 391) where the	
CC	nucleic acid molecule is produced by a process comprising: (a) screening	
CC	a genomic DNA library using as a probe a target sequence defined by any	
CC	of the sequences in SEQ ID NO.1 to 391, identifying members of the	
CC	library which contain sequences that hybridize to the target sequence and	
CC	isolating the nucleic acid molecules from the members; or (b) isolating	
CC	mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid	
CC	molecules whose nucleotide sequence is homologous to amplification	
CC	primers derived from the fragment of the S. pneumoniae genome to prime	
CC	the amplification and isolating the amplified sequences. The computer	
CC	readable medium can be used in a computer-based system for identifying	
CC	fragments of the S. pneumoniae genome of commercial importance, or	
CC	expression modulating fragments of the S. pneumoniae genome. Products	
CC	from the present invention can be used in diagnosis kits and assays, and	
CC	pharmaceutical compositions and vaccines for S. pneumoniae.	
XX		
XX		
SO	Sequence 5365 BP; 1654 A; 960 C; 1082 G; 1669 T; 0 other:	
	Query Match 62.3%, Score 1035.4; DB 19; Length 5365;	
	Best Local Similarity 77.4%; Pred. No. 4.7e-261;	
	Matches 1555; Conservative 0; Mismatches 366; Indels 0; Gaps	
OY	14 TATGCGAAAGAAATCAATTTTCAGCAGATGCGGTCTCCATGGTGGCGAGATTGA 73	
DB		
DB	277 tatgcacaagaataatattcatcatcagtcgccttcagccatgcttcgtcgtgtcga 336	
OY	74 TATGTATGACGATACCGTCGAAGTAACGCTGGTCTTAAAGCGCGCAAGTGTCTTGA 133	
DB		
DB	337 tatcttcgcgcagacacgttaaaagtaaaccttggaccaaaagtcgcaatgctgttcga 356	
OY	134 AAMAGCTTTTGGTCTCCCTTAATTAATTAAGACGGGGTAACATTGCTAAAGATCGA 193	
DB		
DB	397 aaagtcattctcggtcaccccttgattacaaatcaggtgtgcacatttcgcaaaagaatcga 456	
OY	194 ATTAGAAGATCATTTTGAAGACATGGAGCAAAATTTGGTGTCTGAAGTGGCTTAAAC 253	
DB		
DB	457 attggaagaccattcttgaaatatggtgtctaagttagtatacagaagttagctcttcaaac 516	
OY	254 CAATGATATTTGCTGGTGATGGAGACATCTACACAGTTTGACACAGCCATTGTTC 313	
DB		
DB	517 caatgatatcgcgcaggtgaaggaactaaagactcacaacatctctaaccaagcatatgctcgg 576	
OY	314 TGAAGGACTAAAAAATGTGACAGCAGGTGCTATCAATTTGGTATCCGTGAGAGCATTGA 373	
DB		
DB	577 tgaaggaatacaaaaacgtcacagcaggtgccaatccaatccgtattcgtctcgtgattga 636	
OY	374 AACGCAACAGCAACAGCTGTTGAAGCGTTGAAAACCATTTGCTCAACATGTTCTGGCAGA 433	
DB		
DB	637 aacgcagctgtccgcgcagctgtagtcgttgaaaaaacaagcatccctcgttgcacataa 696	
OY	434 GGAAGCATATGCTCAGGTGCGTGTAGATATCATCATACGCTCTGAAAAGTGTGAAGATTTAT 493	
DB		
DB	697 agaagcatatcgcgcagcttgcagcgtatcttctcgtctcgtgaaaaagtttggtagtatac 756	
OY	494 CTCGAAAGCTATGAGCGTGTGGCAACGATGTTGTATTAACATGGAAGATCTCGAGG 553	

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Db 757 ctctgaagcaatgtaaaagttgcaaaagacggtgtatccatccatgaaagatcagctgg 816
OY 554 TATGAAACAGAACTTGAAGTGTGAAGGATGCATTTTGACCGTGTGTCTCA 613
Db 817 tatgaaacagaaagcttgaagtcgtagaagaaatgcaattgacccgtgtacattcaca 876
OY 614 ATACATGTCACAGACAAATGAAATAATGTTGACGACCTTGAAACCCATTATCTTAAT 673
Db 877 gtacatggtgacagatagcgaaataatgtgtcgtccgttgaataatccgttacatttggat 936
OY 674 CAGGATAAAAAGTGTCAACATCCAGACATTTTGCCACTTCTTGAGGAAGTTCTTAA 733
Db 937 tacagacaagaaataatccataatccagaataatcttgcacatttggaaagatcttcca 996
OY 734 AACCAACCGTCTTACTCATTATTGACAGATGTGATGTGATGTAAGCACTTCCAACTT 793
Db 997 aagcaatcgtccacattctgtatctgtcgtatgtgagatgtgagtggtgtcttccaaactc 1056
OY 794 TGTCTTGACAAAGATTCGTGATCTTCAATGTTGATGTTGTTGTTGTTGTTGTTGTTG 853
Db 1057 tgtttgaaacaaagattcgttgaaaccttcaacgttagtagaagcaagcaaccgttcttgg 1116
OY 854 TGATCGTCTGTAAGCTATGCTTGAAGACATTCCTATCTTGACAGGTGTGACAGTATAC 913
Db 1117 tgaecgtgcgaagacatgcttgaagataatcgcacatcttaacagagcgaaacagatcac 1176
OY 914 AGAGATCTAGACTTGAATTAAGATGCTACATGACAGCCCTTGACAGGTGTGCTAA 973
Db 1177 agaagaccttgtcttgcgttgaagatgtgacacatcttgatcgttcaagaagagag 1236
OY 974 GATTACAGTTGATTAAGATACACAGTAAATTTGTAAGTTTGAAGACTTGAAGACTTAT 1033
Db 1237 agtgcacgtgcgaagacagacagcttatttgcagaggtgagtgcaaaatccctgaaagat 1296
OY 1034 TCGTAAACGCTATGACATGATTAATGCAATTTGAACAAACACTTGTGACTTGCACG 1093
Db 1297 ctccacgctgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 1356
OY 1094 TGAATAAATACAAAGATTTGAGGAAAGTGTGAGTGTGAGTGTGATTAACAAAGTAA 1153
Db 1357 tgaataatgcaagaagacgttgcgaatgtgcagaggtgagtgcaaaatccctgaaagat 1416
OY 1154 AGCTCCACAGACAGACGCTTTAAAGAAATGAATACTTCGATGAGATGCTGTAAATGC 1213
Db 1417 agcgcgaactgtaaaactgttgaagaaatgaactgcgcgttgaagatgccttcaacgc 1476
OY 1214 TACACGTGACGCGCTTGAAGAGTATCGTGTGAGTGTGAGTGTGATTAACAAAGTAA 1273
Db 1477 tactcgtgcagctgttgaagaggtatttgcagaggtgagtgcaaaatccctgaaagat 1536
OY 1274 TATGAAAAAGTACAGCTCTTGACCTTGAGGCGCATGATCTACTGACGTAACTTGT 1333
Db 1537 gattcgaagctgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 1596
OY 1334 GCTTGCTGCTCTAGAAAGAGCTGTAGTCAAAATGCTTAAATCTGCTGAGTACAAAGCTC 1393
Db 1597 tctcgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 1656
OY 1394 CGATGTTATTTGACAAGTTGAAANAACGCCCTGCAGAACAGATTTTAATCTGCAACAG 1453
Db 1657 tatcgtatcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 1716
OY 1454 TGAAGTGGTGTATGATTAACAGAAATCATTTACCCCTTCAAAAGTAAACAGATCAGC 1513
Db 1717 cgaatgggttgaatgataatgataatgataatgataatgataatgataatgataatgataatg 1776
OY 1514 GCTTCAAAATGACGCTTCTGTACGTCTTATTTTGAACAAGAGAGTGTGTCTTAA 1573
Db 1777 cctacaaaatgcaatcgttgcagagcttgcgttgcgttgcgttgcgttgcgttgcgttgc 1836
OY 1574 TAAACCTAACCAAGTACGCAAGCCGACAGATGCAAGTATGATTCAGAAATGAT 1633

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Db 1837 taaacagaacacagtaagccacagctccagcaatgataatccagatgatgagcgagatgat 1896
OY 1634 G 1634
Db 1897 g 1897

RESULT 5
AA12979
ID AA12979 standard; DNA; 3625 BP.
XX
AC AA12979;
XX
DT 19-MAR-1999 (first entry)
XX
DE Enterococcus faecalis genome contig SEQ ID NO:42.
XX
KW Enterococcus faecalis; contig; detection; Enterococcal infection;
KM vaccine; attenuation; computer readable medium; ds.
XX
OS Enterococcus faecalis.
XX
PN WO980555-A2.
XX
PD 12-NOV-1998.
XX
PF 04-MAY-1998; 98MO-US08985.
XX
PR 14-NOV-1997; 97US-0066009.
PR 06-MAY-1997; 97US-0044031.
PR 16-MAY-1997; 97US-0046655.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Barash SC, Dillon PJ, Kunsch CA.
XX
DR WPI: 1999-045171/04.
XX
PT New isolated Enterococcus faecalis polynucleotides and polypeptides
PT - used to develop products for the detection of Enterococcus
PT use in vaccines for prevention or attenuation of Enterococcus
PT infection.
XX
PS Claim 1; Page 414-416; 2084pp; English.
XX
CC A computer readable medium has been developed which has recorded on it
CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.
CC AA12938 to AA13919 represent these nucleotide sequences which are
CC primary nucleotide sequences, also known as contigs. The computer-based
CC system can identify fragments of the Enterococcus faecalis genome with
CC commercial importance. The products can be used to detect the presence
CC of Enterococcus faecalis in samples. They can also be used for
CC diagnosing Enterococcal infection in an animal and monitoring
CC progression of disease, and for identifying agents which can be used to
CC modulate the growth or pathogenicity of Enterococcus faecalis, or
CC another related organism, in vivo or in vitro. In particular the
CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
CC can be used in vaccines to prevent or attenuate an Enterococcal
CC infection.
XX
SO Sequence 3625 BP; 1335 A; 542 C; 750 G; 993 T; 5 other:

Query Match 56.7%; Score 942.6; DB 20; Length 3625;
Best Local Similarity 74.2%; Pred. No. 7.8e-237;
Matches 1191; Conservative 0; Mismatches 415; Indels 0; Gaps 0;

OY 15 ATGCAAAAGAAATCAATTTTCAAGACATGCGCTGCTCCATGTTGCGCGAGTGTAT 74
Db 364 atgcaaaaagaaatgtaatttgcagaagatgcagctgacgaatgtacgagatgat 423
OY 75 ATGTTGCAAGATACCGTCAAGTAAAGTAAAGCTTGTCTTAAAGGCGCAATTTTCTTGA 134

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D	424	gataaacagataccagtcgaagatgacattagaccctcaaaagtcgaaagctgtctttagaa	483
O	135	AAACCTTTGGTTTCCTCCCTTAATTAATGAAGAGGGGCTAACCATTTGCTAAAGAGATCGAA	194
D	484	aatacatcttgcctacccttgcattctaccaaagatgagatcaaatgtctaaagaaatttga	543
O	195	TTAGAGATCATTTTGAAGAACATGGGAGCAAAATTTGGTGTGAAGTGGCTCTTAAGCC	254
D	544	cttgaaagatcatcttctgaaaaacatgcygcanaaaatctgattctcgaagtgtctttaaag	603
O	255	AATGATATTGCTGGTGAAGGGACACACTACGCAACAGTTTGTGACAACAGCATTTGCAT	314
D	604	aatgatattctgcgtgagcagacaaacacagcagctgttttgacacaaagcatgttctg	663
O	315	GAAGGACCTAAAAAATGTACAGCAGCGTGCTAAATCCAAATTCGATCCGTCCAGCATTTGA	374
D	664	gaaggtcttaaaaaacgtacacgcgcgagacacacacacattagatcatctgcgtgagattgaa	723
O	375	ACAGCAACAGCAACAGCTGTGAAAGCCTTGAAAACCATTTGCTCAACCTGTATCTGGCAAG	434
D	724	ctagcaacaacaaaacagcagctagaaagaattcaacaattcatctcatctgattgtattcaaa	783
O	435	GAAGCTATTGCTCAGGTGCGTGCAGTATCATCGCTCGAAAAAGTTGGAGATTTATC	494
D	784	gaagcagattgcacaagctgcgcgtcttcaatcaagtgctcgaaaaagtcggcacaattaat	843
O	495	TCGAAGCTATGAGACCGTGTGGCGCAACGATGCTGTGATTTACCTTCGAAGAAATTCAGGT	554
D	844	gcgcagtcgcaatgysaaaaagcttcgttaacagcagcggtatattacattctgaaatcaaaag	903
O	555	ATGGAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAA	614
D	904	attgaaaacagaattctgactgtgtttgaagaaatgcacaattcgcgcggttattattctcaa	963
O	615	TACATGCTACAGCAATGAAGAAAATATGTTGCGACGCTTGAAAACCATTTATCTTAATC	674
D	964	tactgtgttaactgcgaatacgaataaaatgysaagctggttttagaaaaatccatatcttaact	1023
O	675	ACGGATTAATAAAGTGTCAACATCCAAAGACATTTTGCACATCTTAGAGAAATTCTTAA	734
D	1024	accgacaaaaaaatccataatctcaagatatcttaccattatagaaacaaatcttcacaa	1083
O	735	ACCAACCGTCCATTTACTATTTATGCAATGATGATGATGGTGAAGACATTTCCAAACCTT	794
D	1084	caaaagcgcctccactatgattctatctgcgattgagtgtgtgysagagcttcaacaaatla	1143
O	795	GCTGTACAACAATAATTCGCGAGTACTTCATATGTCGTTGCTGTCAAAAGCGCAGATTTGGT	854
D	1144	gtatctgaaacaaaatccgcgysaaatctttaaagctgtgcgaatgaatgaagcgcaggaatttctg	1203
O	855	GATCGTGTAAAGCTATGCTTGAAGACATTTGCTATCTTGACAGGTGGTACAGTATTA	914
D	1204	gaccgcgcgaagaagcgaatctgtgaagatattgtctattttaaagctggttaacagatcaact	1263
O	915	GAGGATCTAGGATTTGAAGATGCTACAAATGAAGACCTTTGGACAGGGCTGTGAAG	974
D	1264	gagcactttaggttagtgattgaagaagcaacactatgtgaaccttagaaacttagaaactgtgcaaa	1323
O	975	ATTACAGCTTGAAGAGATAGCAACGTAATTTGTTGAAGGTTACAGAACTTATGACGTATT	1034
D	1324	gtatgtctgcgaacaagaataaacacaaatgttcgaaagctgtctgttcaaaagaagacat	1383
O	1035	GCTTAACCGTATTGCATGATTTAAATGCAATTTAGAAACMACAACTTTGACTTTGACGT	1094
D	1384	gagccgcgcgtctcatcttaattataaaaacaaatctgcgcgaacaaacgctcatgtatttgcgt	1443
O	1095	GAAAAAATCTCAAGAACGTTTGGCAAAATTTAGCGGTGCTGTAGTGTATTCAAAGATAGA	1154
D	1444	gaaaatactcaagaaacgcttttgccaaattcagctgtgysgtgtcgttcgtttaaagtcggt	1503
O	1155	GCCTCAACGAGACAGCTTTTAAAGAAATGAACCTCCGATTGAGATGCTCTAAATGCT	1214
D	1504	gtcgcgaacgcgaacgaattttaaagaatttaaaattacgaattcttgaagtgatlaacgaa	1563

[illegible]

RESULT	6	
AAAT69201		
ID	AAAT69201	standard; DNA, 1647 BP.
XX		
AC	AAAT69201:	
XX		
DT	20-AUG-1997	(first entry)
XX		
DE	Lawsonia intracellularis GROEL DNA.	
XX		
KM	Intestinal disease; porcine proliferative enteropathy; vaccine;	
XX	GROEL; heat shock protein. ss.	
OS	Lawsonia intracellularis.	
XX		
PN	NC9720050-A1.	
XX		
PD	05-JUN-1997.	
XX		
PF	29-NOV-1996;	96MO-AU00767.
XX		
PR	30-NOV-1995;	95AU-0006811.
XX		
PR	30-NOV-1995;	95AU-0006910.
XX		
PA	(DARA-) DARATECH PTY LTD.	
XX	(PIGR-) PIG RES & DEV CORP.	
PI		
XX	Hasse D, Panaccio M;	
DR	WP1: 1997-310605/28.	
XX		
DR	P-PSDB; AAM16678.	
XX		
PT	Vaccine for treating or preventing Lawsonia intracellularis	
XX	Infection - especially in pigs, containing non-pathogenic form of	
PT	bacterium or its components	
XX		
PS	ClaIm 12; Page 38-42; 94pp; English.	
XX		
CC	A DNA molecule (AAAT69201) codes for the GROEL heat shock protein	
CC	AA1665678) of Lawsonia intracellularis, the causative agent of porcine	
CC	proliferative enteropathy (PPE). A genomic library was prepd. from	
CC	L. intracellularis PPE lesion isolates and screened with rabbit	
CC	anti-L. intracellularis antiserum. Phagemid DNA was isolated from	

[illegible][illegible]



XX (DARA-) DARATECH PTY LTD.  
PA (PIGR-) PIG RES & DEV CORP.  
PI  
PI Haase D, Panaccio M;  
DR WPI. 1997-310605/28.  
XX  
XX Vaccine for treating or preventing Lawsonia intracellularis  
PT infection - especially in pigs, containing non-pathogenic form of  
PT bacterium or its components  
PS Claim 14; Page 47-50; 94pp; English.  
XX  
XX DNA molecules (AAT69203-15) were isolated from an immunoscreening of  
CC a Lawsonia intracellularis library using experimental sera from  
CC vaccinated pigs. These nucleic acids, as well as isolated GroEL,  
CC and GroES (AAT69201-02) sequences, encode putative vaccine candidates  
CC (see also AAM16678-85) useful for protection of animals and birds  
CC against intestinal diseases, esp. protection of pigs against  
CC porcine proliferative enteropathy (PPE). They can also be used as  
CC genetic vaccines.  
XX  
SQ Sequence 4972 BP; 1717 A; 871 C; 831 G; 1532 T; 21 other;

Query Match: 42.4%; Score 704.2; DB 18; Length 4972;  
Best Local Similarity 66.4%; Pred. No. 2,1e-174;  
Matches 1044; Conservative 0; Mismatches 523; Indels 6; Gaps 2

OY 19 CAAGAACAATTTCACGACAGATGCCTGTGCCATGTGGCGGAGTTGATATGT 78  
DB 2055 cttaagaatacccttttgcatacgaagcccgtgaaaaacttcacgaaggctgataaac 2114  
OY 79 TAGCAGATATCCGTCAAAAGTAACGCTGTGCTTGAAGGCGCATGTGTTTGAAAAAG 138  
DB 2115 ttgcaaatcgctgtaaagtataaccacttgggcccaaagggcgtatgctgatgaaagt 2174  
OY 139 GTTTTGCTTCCCTTAATTACTAATGACGGGGTAACCATTTGCTAAAAGATGAAATAG 198  
DB 2175 ctttttgtccccccgtattcatcaaaaagatggtatctgttgcaaaaagaattgacctg 2234  
OY 199 AAGATCATTTTGA AAAACATGAGAGCAAATTTGTTGTTGAAGGCTTTATAAACCATG 256  
DB 2235 agataataagttggaataataatgtagcgccaataatggtlaaagaagtagtcccaaaactg 2294  
OY 259 ATATTGCTGTGATGAGGACGACTACTGCAACAGTTTTTGACACAAGCAATTTGTCATGAG 318  
DB 2295 atattgcgtgtagatggaactcatacacgacaacagtcctctgacaaagtatttcgtgag 2354  
OY 319 GACTATAAAATGTATCACAGAGGTGCTAATCATCATTTGGTATTCCTCGACGATTTGAACAG 378  
DB 2355 gtgtaaaactctgtagacgctgtgcgtaatccctatgcatatgaacgtgcatagtaag 2414  
OY 379 CAACAGCAACAGCTGTGAGACCCTTGAAGCCATTGCTCAACTGTATTTGCGACAAGAG 438  
DB 2415 cgtgtgtgtcgttatacctaagaactaaggaatatacctaagaactctctgtgaccaaaag 2474  
OY 439 CATATGCTCAGAGTGCCTGCAGTATCATCCAGCTGTGA--AAAGTTGAGAGTATATCT 495  
DB 2475 aaatgagctcaagttcggaacacattctgcacaactctgtatacacaatagttaatcatag 2534  
OY 496 CAGAAGCTATGAGACGTGTGGCAACGATGGTGGATTTACCATCAAGAAATCTCGAGSTA 555  
DB 2535 ctgaagctatggtctaaagttcgaaaaaggaagggtgatacaacaagttcggaagtagtaagtc 2594  
OY 556 TGGAAACAGAACTGAAGTGGTTGAAGACGCAATTTGACCGCTGGTTACGTCTCAAT 615  
DB 2595 ttgaaactacactagatcgtgttgaaagaaatgaaagttcgacgctggtacccctccatc 2654  
OY 616 ACATGGTACACGAATGAAAAAATGGTTGGCAAGCTGAAAGAACCATTTATCTTAAATCA 675  
DB 2655 accttgtaactaaactccgagaaaaagtggttttgtaacctgtgaactgaacctatccctattcgta 2714

QY	676	CGGATGAAAAAGTGTGCTAAACATCCAAAGCAATTTTGGCAGCTACTGTGAGAACTTCTTTAAA	735
Db	2715	atgagaaaaagatctactagcagaagaacagcagctaccacactcttaagaacaaatctgcaaa	277
QY	736	CCAACCGTCCATTACTCATTTATGTGCAGATGATGTGATGGTGAAGCACTTGTCCAACCTTGG	795
Db	2775	taaacgcctcaaccctctatctatctgtgaagacgtagaaggtgaagcacttgcacaaccttg	2834
QY	736	TCTTGACCAAGATTCGTGTGTACTTTTCAATGGTGTCTGTCCAAACGGCAGAGATTGGTG	855
Db	2835	tagcaataaagctccgcttggagcactcccaagctgttagcgcgttaaaagctcccggtcttggcg	2891
QY	856	ATCGTGTAAAGCTATGCTTGAGACATTCGCTATCTTGACAGGTGTGACAGTATTAACA	915
Db	2895	aacgcgttaagactatgctctgaagatatctgctaccctctactcgtgaagaaagcaaatattg	2954
QY	916	AGGATTCAGACACTGTAATTTAAAGAATCTCAATGTGACACACCTTGTGGACAGCTCTAAGA	975
Db	2955	aagctcggtgtataaagctctgaagaaatglaagctgtcctctcttagaacacgttaaacgtg	3014
QY	976	TTACAGCTGTTAAAGTATACCAAGATTTGTGTGAAGCTGACGAAGTTCAGAGATTTTG	1033
Db	3015	tagtatacttgcagaagaataactctactacgtctgaatgtgttgcgtgaagaaacagaagatatta	3072
QY	1036	CTAACCGTATTCGACTGATTTAATTCGCAATTTAGAAACAACATTCCTGACTTTGACCGTG	1095
Db	3075	aagctcgagttacaacaaatctgtcacaaatctgaagaacaagctccagatattatgacctg	3134
QY	1096	AAAAACGTACAAAGACGTTTGGGGAATTTACTCGTGTGTGTACTGTCTTATCAAGTTGAG	1155
Db	3135	aaaaactctcaagaagctctgtcacaactctgttggtagtagcgttatccaagttggag	3194
QY	1156	CTCCACAGACAGACGCTTTAAAGAAATGAACCTTGCATTGAGAGTCTCTAATGCTA	1215
Db	3195	ctgtactatgaactaaatgaagaagaagaagatctgttgaagaatgctcttaaatgcaa	3254
QY	1216	CACGTGACGCGCTGTAAGAAGCTATCGTGTGTGTGTGGAACAGACACTTATACGGTTA	1275
Db	3255	caagagctggtgtgaagaagatctgtccctgtgtgtgtgtatcgtcttctgtcgtcca	3314
QY	1276	TTGAAAAAGTAGCAGCTCTTCAAGCTTGAAGGCGATGATG--CTTACTGACGTATACATPG	1333
Db	3315	ttaaagtctcttgatgatcttaaacctgtgatgatgaatgaacttgcgtgaacttaatatca	3374
QY	1333	TGCTGTGCTGTCTAAGAAAGCTGTAGCTCAATTTCTTTAAATGCTGGGTAGAGAGCT	1392
Db	3375	tcgctgctctctcttgagaagcctttagctcaaatctgtgcgaatgctgcgtctatgaagct	3433
QY	1393	CCGATGTTATTCACAAGTTGAAAAACAGCCCTGACGAAGCAAGATTATATGCTGCAACG	1453
Db	3435	ctatgtctgtgagaaaaagctctgtgaaccaaagaatggtcttggaattcaatgcgtcacg	3494
QY	1453	GTCAGTGGGTATGATGATTTAAACAGAGATCATTCAGCCGTCTCAAGATCAAGATTCAG	1512
Db	3495	gagaatactgaagaccttatctaaagcgtgtcattgacttaccctaaaaaagttacaagattg	3554
QY	1513	CGCTCAAAATGACACTCTTCTACTACGTAGCTTATTTTGTGACAAAGAGAGCTTGCTCA	1572
Db	3555	cattacaataatgacacatcagtgagctccctctactcttaactacaagaatgtcgcatatgctg	3614
QY	1573	ATTAACCTCTAACC 1585	
Db	3615	aaaaaccagaacc 3627	
RESULT 8			
AAAF28548			
ID AAF28548 standard: DNA, 96109 bp.			
AC AAF28548:			
DT 04-APR-2001 (first entry)			

Query Match	39.48;	Score 654.2;	DB 22;	Length 96109;
Best Local Similarity	63.48;	Pid. No. 8,5e-161;		
Matches 1036;	Conservative	0;	Mismatches 593;	Indels 6;
			Gaps	
Q15	ATGCGAAAGAAATCAATTTTCACGACGATGGGTCTCCATGTGGCGAGTTGAT	74		
Db 49276	atggcaaaagctgaagcttttgcctcaaatcccggaataaattgattgattgattcaac	49335		
Q75	ATGTTAGCAGATACCGTCAAGTAACGGTGTGCTTAAAGGCGCATGTTGTTGAA	134		
Db 49336	attcttgcgagctgctgcaagttacacctagtgctcaaaagccgcgaatgattgattac	49395		
Q135	AAAAGTTTGGTTCTCCCTTAATTACTAATACGGGGTAACATTGCTTAAAGATCGAA	194		
Db 49396	aaatcattcttgctgcgcgcacccatcccaagaatgctgctgcagttgcttcaaaagattgaa	49455		
Q195	TAGAAGATCTTTTGAACACATGGGACCAAAATGGTGTCGAAGTGGCTTAAAC	254		
Db 49456	cttggaagtaatttgaaaaaacttggctgacaaattgctgctggaagttgcttccaaagac	49515		
Q255	AATGATATGTGCTGATATGGAGCAGTACTGCAACAGTTTGAACAAGCATTGTTCAT	314		
Db 49516	aattgctggaagcgatgaaacaacacgcgaacagtaactgtccaaagcatcttglt	49575		
Q315	GAAAGACATAAAAAATGTGACACAGTGCTTAATCAATTGTGATCCGTCAGACATTGAA	374		
Db 49576	gaaggcaagaanaagcttgcgcgaagcatgatactaaatgactaaagcgtgattgattac	49635		
Q375	ACAGCAACAGCAACACTGTTAAACCTTGAAGCATTGCTCAACCTGTATCGGAAG	434		

[illegible]

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OY 1509 TCAGCGCTTCAAAATGACGAGCTTCGTAGTACGTCATATTGTTGACACAGACAGACTTCCT 1568
Db 50776 tccgcatcttgaaacacgctgcctctgtctgcagagttctgagcttgcaccactgagtgatc 50835
OY 1559 GCTTATTAACCTGAACGACTACGCCACGCCACGACGATGTCAGAGTATGATCCAGGA 1628
Db 50836 accgataaacacgacccgacgaagcaccacatgcccagcaggtgtgtatcgtgtatcgtgt 50895
OY 1629 ATGATGCTGGCGATG 1643
Db 50896 atggcggtatgatg 50910

RESULT 9
AAK86152
ID AAK86152 standard: DNA, 1665 BP.
XX
XX AAX86152:
XX
XX 22-SEP-1999 (first entry)
XX
XX DNA encoding a Streptococcus pneumoniae heat shock protein (Hsp)60-1.
XX
XX Heat shock protein: Hsp60-1; Immune response; immunological carrier;
XX cancer control; tumour; sarcoma; cancer; gene therapy; ss.
XX
XX Streptococcus pneumoniae.
XX
XX MO9935270-1.
XX
XX 15-JUL-1999.
XX
XX 29-DEC-1998; 98MO-CA01203.
XX
XX 31-DEC-1997; 97US-0001737.
XX
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
XX Mizen L, Walslewski J;
XX
XX WPI: 1999-430397/36.
XX
XX DR P-PSDB; MAY23901.
XX
XX PT New nucleic acid encoding heat shock protein-60 from Streptococcus,
XX agents and for diagnosis
XX
XX PS Claim 3; Fig 1A-B; 176pp; English.
XX
XX
XX The present sequence encodes a heat shock protein, designated Hsp60-1.
XX The protein, its fragments, variants and fusion proteins, are
XX used to elicit or enhance an immune response against Streptococcus,
XX and to elicit a similar response to a target antigen fused to the
XX protein. Unlike other immunological carriers, Hsp60 proteins are not
XX immunosuppressive so provide an increased response to any conjugated or
XX fused antigen. Also, where used for cancer control, they lack the side
XX effects associated with endotoxins. They can also be used to detect
XX specific antibodies and in treatment or prevention of tumours
XX (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or
XX liver). The Hsp60 polynucleotide is used for recombinant production
XX of the protein, as a source of primers and probes for detecting
XX streptococci in standard hybridization/amplification assays, and
XX therapeutically in gene therapy vectors.
XX
XX Sequence 1665 BP; 438 A; 401 C; 480 G; 346 T; 0 other;

Query Match 35.6%; Score 590.6; DB 20; Length 1665;
Best local similarity 61.4%; Pred. No 7.4e-145;
Matches 1001; Conservative 0; Mismatches 619; Indels 9; Gaps 3
OY 1 GATTTCGGCTTCATAT---GGCAAAAGAAATCAATTTTCAGCAGATGCGCTGCTGCA 57

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Db	1	gaatttcgcttcataatgagcgtaaaagcgtlaaaatcgtgtaagaaagcgtctgtgtgaaaa	60
OY	58	TGTCGCGGGAGTTGATATGTTACGATACCTCAAGTAAACCTTGGTCTTAAAGGC	117
Db	61	tgtctcgcgaggtlaaaagtaacgagcaatcgaatgaagttaccccttcggcccaaaagc	120
OY	118	GCAATGTTGTTCTTGAAAAAGCTTTTGGTTCTCCCTAATTACTAATGACGGGGTAACA	177
Db	121	gtaacgtagttcttgtaaaatccttcgtgtcacgcgcatacctaagaatgtgttcgcg	180
OY	178	TTTCCTAAAGAGATGAAATTAAGAAGTCATTTTGAAGATGAGGCAAAATGTGTCG	237
Db	181	tgcacgtggaatcgcgaatcgcgaagaacaagttcgtaaaacaatgtgtgcgacgaatgtgaaag	240
OY	238	AACTGGCTTCTTAAACCAATGATATTCCTGCTGATGAGCAGCATCTGCAACATTTTGA	297
Db	241	aaatttgcctctaaagagaaacgcgcgtcgaagtgtacggtacacacacgcgcgaacgttactgt	300
OY	298	CACAGACCATGTGTTCATGTAGAGACTTAAAAATGTGACAGCGAGTCATTCATGTGTA	357
Db	301	ctcagtcatactactgtaagggccttgaaagcgtgtgtcgtgcggtatgaaacccgatatc	360
OY	358	TCCGTGAGGCAATGAAACAGACCAACAGCTGTGGAAGCCTTGAAGCATTTCTC	417
Db	361	tgaaaagcgtgatacgcgaagaagctgtcgtcgtcgttctgtgaagaacgtgaagaacgttcgcg	420
OY	418	AACTGTATCTGCGAAGAAAGCATTTGCTCAGGTGCGTCAGTATCATCAGCTC--TTG	474
Db	421	tacgcgtcgcgaatcctaagactatgtctaagttgtgatacatcgcgttaactcgcga	480
OY	475	AAAAAGTTGAGAGATTATATCCAAACCTTGTGAGACGTGTGGCAACGATGTGTGATT	534
Db	481	aaacgcgtgtgataacgtatcgtcgtgaagcgtatgaaacgaatgcgtgtaagaagcgtgtc	540
OY	535	CCATGGAAGATCTCGAGGTATGAACACAGAACTTGAAGTGTGGAAGCATGCAATTTG	594
Db	541	cagtttgaagaaggttacaggtctcgaagacgaacgtgaaagcgtgtgttgaaggtatgaaagttcgc	600
OY	595	AACGATGTACTGTCTCAATACATGGTGCACAGACATGAAGAAAAAGTGTGACAGCTTG	654
Db	601	accgtggtaccggtctccttacttctacaacagcggaaacgtgcgagtagaatgtg	660
OY	655	AAAAACCCATTATCTTAATCAACGGATPAAAAAGTGTCAACATCCAGAACATTTTGGCAC	714
Db	661	aaagccggtctcctcctggtcgtgtacaaagaaatcccaaacatccgcgaaatgtctgcg	720
OY	715	TACTTGAGAGATTCTTAAACCAACCGTCCATACTCATTTATTCAGATGATGTGATG	774
Db	721	tctctgaagcctgaagaaagcaagcaaacgcgtctgtatcatcgtctgaagaatgttgaag	780
OY	775	GTAAGACACTTCCAAACCCCTTCTCTTGAAGAAATTCGATGACTTTCATATGCTGTCTG	834
Db	781	ggaagacgctgtgaaactcgtgtgttaaacacatgcggtatcgttaaaagtcgcgcg	840
OY	835	TCAAAAGCGCAGATTGGTATATGCTGTAATGCTGTAATGTAAGACATGCTATCTTGA	894
Db	841	ctaaagcaaccgtcttcggtgcgtacgtctgttaaaagcaatgcgcgcgtatcgcgtacccgta	900
OY	895	CAGGTGTACAGTATTACAGAGATCTAGAGATCTGAATTTAAAGATGCTCAATGACAG	954
Db	901	ccggtgtgtaccgttatcctctgaagaaatcgtatgtatgtgagcctgaaaagcaactctgaaag	960
OY	955	CCCTTGGACAGCGCTGCTAAAGTTTCAAGTTGATPAAAGATACACAGTAATGTGTAAAGTT	1014
Db	961	actcgtggcgaagsgaaacgctgtgtatatacaaaagataaccaccccatcatcgtatgtgcg	1020
OY	1015	CAGGAAGTTACAAAGCTATTTCTTAACCGTATTCGACATCGATTTAAATTCGCAATTAAGAACAA	1074
Db	1021	tgggtgagaagaagcgtcaatccaaagtcgtgtgaaccagatcttcagcgaagcgaagaag	1080
OY	1075	CAACTTGTGACTTGTGACGCTGAAAAAATCTCAAGAAACGTTTGTGGGAATTTACTGTGTGG	1133



[illegible]

AAAC90805 ID AAC90805 standard; DNA; 1647 BP.  
XX AC AAC90805;  
XX  
XX  
XX 16-MAR-2001 (first entry)  
DE Escherichia coli GROEL nucleotide sequence SEQ ID NO:2.  
XX  
XX Escherichia coli; GROEL; mutant; mutain; Improved stability;  
KW chaparone; nootropic; neuroprotective; Alzheimer's disease;  
XX prion disease; Creutzfeldt-Jacob's disease; CJD; ds.  
OS Escherichia coli.  
XX  
XX WO200073463-A1.  
PN  
PD 07-DEC-2000.  
XX  
XX 26-MAY-2000; 2000WO-CB02019.  
PF  
XX 27-MAY-1999; 99GB-0012445.  
PR  
XX  
XX (MED1-) MEDICAL RES COUNCIL.  
PA  
PI Buckle AM, Fersht A;  
XX  
XX WPI: 2001-061543/07.  
DR P-PSDB; AAB50536.  
XX  
XX Novel GroEL chaperone polypeptide, its homologue or fragment comprising  
PT modifications in specified amino acid residues of GroEL protein  
sequence, used to treat diseases associated with protein/polypeptide  
PT structure

Disclosure: Page 47-49; 56pp; English.

XX  
XX The present invention describes a GroEL chaperone polypeptide (CP) (I),  
CC its homologue, or fragment having protein refolding activity, and  
CC comprising one or more amino acid modifications at any one of amino  
CC residues 207, 212, 217, 223, 233, 267, 271, 294, 305, 308 and 326 of the  
CC fully defined GroEL protein sequence given in AAB50536, or their  
CC equivalent positions in other homologous CPs. (I) can have neurotropic and  
CC neuroprotective activity. (I) can be used in therapy (i.e. gene  
CC therapy). (I) is used in the manufacture of medicament for treating a  
CC disease associated with protein/polypeptide structure. (I) immobilised to  
CC a solid phase, on contact with a molecule/reconstructions it, in which the  
CC molecule is subjected to inactivation or denaturation prior to contact  
CC with (I). The solid phase is a chromatographic matrix and the contact of  
CC the molecule and (I) is carried out by applying the molecule to the top  
CC of a bed of the matrix packed in a column and then eluting the molecule  
CC through the column. (I) is useful for altering the structure of a  
CC molecule by folding, unfolding or refolding. Preferably, the  
CC stoichiometry between the chaperone (I) and the molecule being altered  
CC is about 1:1. (I) is also useful for purifying or increasing the yield,  
CC specific activity and/or quality of biological molecules. (I) can also  
CC be used for treating a animal or human patient suffering from a disease  
CC associated with protein or polypeptide structure. The polypeptides when  
CC administered either directly or via nucleic acid constructs may be  
CC useful for treating Alzheimer's disease and prion diseases including  
CC Creutzfeldt-Jacob's disease. The mutant or modified polypeptides have  
CC increased stability while retaining full chaperone activity. The present  
CC sequence encodes the Escherichia coli GroEL chaperone, which can be  
CC modified for use in the present invention.  
XX  
XX Sequence 1647 BP; 437 A; 394 C; 477 G; 339 T; 0 other;

Query Match 35.5%; Score 589.8; DB 22; Length 1647;  
Best Local Similarity 61.3%; Pid. No. 1.2e-144;  
Matches 986; Conservative 0; Mismatched 617; Indels 6; Gaps 2.

18 GCAGGAAGAATCAATTTCGACGAGATGGCGGTCTCCATCGTGCAGCAGATTGATGATG 77

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Db      7 gctaaagcgttaaatcgtgtaacggtcgtgltgtaaatgctgcyggtlaaacgtla 66
Oy      78 TTAGCAGATACCGTCAAGAGTAACGCTTGCTTAAGAGCGGCAATGTTGTTGAAAA 137
Db      67 ctggcaatcgtcaagtaaatcctcgtctcaaaagcgctgaagcttctgtatataa 126
Oy      138 GCTTTGTTCTCTCTTAATTAATGACGGGTAACATTCCTTAAGAGTGAATTA 197
Db      127 tcttcgtgacacgcacatcccaagaagtggttctcgttctgltgtaaatcgaactg 186
Oy      138 GAAGATCATTTTAAATAATGGAGCAAAATTTGTTGTTGAGTGGCTTTAAACCAAT 257
Db      187 gaagacaagltcgaaaaataatggtgctgagatggtgaaagaagttgctctcaagaac 246
Oy      258 GATATTGCTGATGGAGGAGCTACTGCAACAGTTTGAACAGCCATGTTGTCATGAA 317
Db      247 gacgtcagcgagcggtatccacacacgtgtaacgttactggtcgaagctatcaacgtgaa 306
Oy      318 GGAATAAAAAATGTGACAGCAGTGTCTAATCAATTGTTGCTGAGGCAATTTGAACA 377
Db      307 ggtcgaagaagcgtgtgctgagcggaatgaaccgtgtaacgtgaaacgtgatacgaacaa 366
Oy      378 GCAACAGCAACAGCTGTTGAAGCCTTGAAGCCATGTCACCTGTAATCTGGCAAGAA 437
Db      367 gctgtaccgctgacgttgaagaactgaagcgctgtccgtacatgctctgactcaaa 426
Oy      438 GCTATTGCTCAGTGGTGGCAATCATCAACGCTC---TGAATAAGTTGAGAGTATATC 494
Db      427 gctgtgtcgaagtggtgtacatccatccgttaactcgaagaacgtgtgaaactgatac 486
Oy      495 TCAGAAAGTATGAGAGCTGTGGGCAACAGATGTTGTTGATTCACATGAGATTCGAGGT 554
Db      487 gctgaagcgtatgaaagaagtcgtlaagaagcggtatcacacgtgtgaaagcggtacccgt 546
Oy      555 ATGGAACAGACAGCTTGAAGTGTGAAGGATGCAATTTGACCGGTGTACTGTCTCAA 614
Db      547 ctgcaggaagaaactggaagcgtgtgaaagtaagcagctgcaagcggtcaccgttctct 606
Oy      615 TACATGCTACAGACATGAAAAATGTTGACAGCTTGAAGAACCATTTATCTTAATC 674
Db      607 tactatcaacaagccggaacatcgtgagcagtagaacgtgaaagccgttcatccgtcgtg 666
Oy      675 ACGATAAAAAATGTCAACATCAACAGATTTTGCACACTGTGAGAGTCTTAATA 734
Db      667 gctgaagaagaatctccaacatcccggaatgctgcggttccggaagcgtgtgcaaa 726
Oy      735 ACCAACCTCCATTAATCAATTTGCAATGATGATGATGATGATGATGATGATGATGAT 794
Db      727 gcaagcaaacgcgtgcatcaltcgtgaagatgaaagcggaagcgctggaactctg 786
Oy      795 GTCTTGAACAAGATTCGTGTAATTTCAATGATGATGATGATGATGATGATGATGATGAT 854
Db      787 gttgttaacacatcggtgcatcgtgaagcggtggttaagagccggtcctcggtc 846
Oy      855 GATGCTGTAAGTATGCTTGAAGACATGCTGATCTGACAGGTGATGATGATGATGATGAT 914
Db      847 gctgcgtgaagaactgctgcaagcgtatcgaacccgtgacgtgctgactgctct 906
Oy      915 GAGGATCTAGACTTGAATTTAAAGATCTCAATGACAGCCCTGAGAGGCTGCTTAAG 974
Db      907 gaagagatcgtatgagcgtggaagaacacccctggaagacactggttcaagcctaaagc 966
Oy      975 ATTACAGTGAATAAGTAGACAGTAAATTTGTAAGGTTACAGAACTTACAGAACTTAT 1034
Db      967 gttgtgtatcaacaagaacacacacacatcaltcgtggtgtgaagaagcgtatcgaatc 1026
Oy      1035 GCTAACCGTATGCTACTGATTAATCGCAATTAAGAAACACACTTCTACTGATTAACGCT 1094
Db      1027 caagcggtgtgtgtcagatcgtcagcagatgaaagaagcaactctcagcaagcgt 1086
Oy      1095 GAAAACTACAGAGCTTTGGCGAAATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1154

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Db      1087 gaaaacatcgaggaacgcgtatgcaaacctgcaagcggtgtgacgttatcaaaagtggt 1146
Oy      1155 GCTCCAAACGACAGACAGCTTTTAAAGAAATGAACCTTGGATTGAGAGTCTTAATGCT 1214
Db      1147 gctgcacacgaagttgaaatgaagaagaaaaaacgacgcttgaaagatgcccctgcaagc 1206
Oy      1215 ACACGTGACGCGGTGGAAGAGTATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1274
Db      1207 acccgtgctgagtgaaagagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1266
Oy      1275 ATTGAAAAAGTAGACAGCTTCTGAGCTTGAAGGCGATGATGCTACTGACGTACAA--TT 1331
Db      1267 gactcaaacctggtcgtacacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1326
Oy      1332 GTGCTTGTGCTGCTGTAAGAGAGCTGTACGTCAATGCTTTAATGCTGAGGATGAGAGG 1391
Db      1327 gactcgtgtcaatgaaagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1386
Oy      1392 TCCGTGATTATTTGCAAGTTGAATAAACACGCCCTGCAAGACAGATTTAATGCTCAACA 1451
Db      1387 tctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1446
Oy      1452 GGTGAGTGGTTGATGATTAATTAACAGAAATCATTTGACCTGTCAAGATGACATCA 1511
Db      1447 gaagaaatcggcaacatgacatgacatgacatgacatgacatgacatgacatgacatgac 1506
Oy      1512 GCGCTTCAAAATGCAAGCTTCTGTAGCTTATTTGACAGAGAGAGTGTGCT 1571
Db      1507 gctcgtgacgtacgagcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1566
Oy      1572 AATAAAGCTGACAGCTTACGCCAGCGCCAGCAATGCCAGCAGGTATG 1620
Db      1567 gacctgcgaaaaacgatgacgtactgaagcgtcgtgtgtgtgtgtgtgtgtgtgtgtgt 1615

RESULT 12
AAA48500
ID AAA48500 standard; DNM: 4524 BP.
XX
XX AAA48500;
XX
XX 07-DEC-2000 (first entry)
XX
XX Escherichia coli groES, groEL and tlg operon coding sequence.
XX
XX E. coli; groES, groEL, tlg; proOmpa; trigger factor;
XX outer membrane protein Ompa; expression plasmid; ds.
XX
XX Escherichia coli.
XX
XX EP1016724-A2.
XX
XX 05-JUL-2000.
XX
XX 28-DEC-1999; 99EP-0126094.
XX
XX 28-DEC-1998; 98EP-0372965.
XX
XX (HSPR-) HSP RES INST INC.
XX
XX Sogo K, Yanagi H, Yura T;
XX
XX MPI: 2000-414804/36.
XX
XX Novel operon comprising genes encoding a trigger factor, GroEL and
XX GroES, useful for recombinantly producing foreign proteins -
XX
XX Disclosure: Page 16-19; 24pp; English.
XX
XX The present sequence is the coding sequence of an artificial operon
XX comprising the groES, groEL and trigger factor genes of Escherichia coli.
XX GroES is a protein which is involved in the folding of proteins, along
XX with GroEL. The trigger factor is involved in the transportation of

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XX WPI: 1999-081217/07.  
XX  
XX  
XX New isolated *Borrelia burgdorferi* nucleic acids - used to develop  
PT products for the detection, diagnosis, characterisation, prevention  
PT and therapy of infections, particularly Lyme disease  
XX  
XX  
PS Claim 1: Page 157-671, 1128pp: English.  
XX  
CC AAX20246 to AAX20402 represent polynucleotide sequences isolated from  
CC *Borrelia burgdorferi* (Bb). Products derived from Bb can be used for  
CC the detection, diagnosis, characterisation, prevention and therapy of  
CC Bb infections, e.g. Lyme disease. They can also be used for the  
CC production of biosynthetic products, e.g. enzymes. *Borrelia* belongs  
CC to a family of motile, spiral-shaped bacteria called Spirochetes.  
CC Spirochetes are pathogenic in humans and *Borrelia* causes epidemic and  
CC endemic relapsing fever, and Lyme borreliosis, more commonly known as  
XX Lyme disease.  
XX  
SO Sequence 910715 BP: 327171 A; 129646 C; 130753 G; 323091 T; 54 other;

[illegible]

OY	727	TTCCTAAACCAACCGTCCATTAAGCATATTGCAATGTGATGGTGATGAAGCACTC	786
Dd	221516	TTTTAGGCAATAAATACCCTTTATTAAATATGCTGTGAGATATTAGGGGGATGCTCTTG	221457
OY	787	CMACCCTGTCTTGAAACAAGAATCTGTACTTTCAAATGTGTCTGTCAAAAGCCGAC	846
Dd	221456	CTGCTCTTGTTTAAAAACACCGCTTAAGAGAGCTTTTAAAAGTAGTGTCAATTAATCTCTG	221397
OY	847	GATTGGTGATCGCTCAAGCTATAGCTTGCAACATGCTATCTTGACAGAGTGGTACAG	906
Dd	221396	GTTTGGTATACGACAAAGAACATGCCTGAGATATGCAAGTGTACGCCGCTGTT	221337
OY	907	TGATTNANGAGATCAGACACTGAAATTTAAAAGATGCTACATGACAGCCCTTGGACAG	966
Dd	221336	TAAATCATGGAGGAGCTGAGCCCTTACTCTTGAGACAGTTGAAATGAGCAACTGTGACAGG	221277
OY	967	CTGCTAAGATTACAGTTGATTAANAAGTATAGCACAGTAAATGTGNAAGTTCCAGAGTTCAg	1026
Dd	221276	CTAAATCATTTAAGTTGATTAAGACAAATACCACTATTATTA --TACCGGCAATPAAG	221220
OY	1027	AAGCTATTGCTAACGGTATFAGCTAGATTAATTCGAAATTAGAAACAAACACTTCTACT	1086
Dd	221219	AGCAAAATAAAGAGGCTTCAGAGCTTATTAAAAAGCAATTGAAAGATTCAACATCTTAAT	221160
OY	1087	TTGACCGTGAATACTACAGAAGCTTTGGCGAAATTAAGCTGTGTAGCTGTATCA	1146
Dd	221159	ATGATTAAGAAAACTTCAAGAGGCTTCCAAAACCTTTGTGGCGAATTTCTGTATTA	221100
OY	1147	AAGTAGAGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACCTGGCAATAGAGATCTC	1206
Dd	221099	ATGTTGGAGCTGTACTAGGTAGAGCTTAAGAGAAAAAGATAGATTAGACACCTC	221040
OY	1207	TAAATGTCACAGTGCAGCCCTTGAAAGAGTATGCTGCTGTGTGTGAAACAGCACTTA	1266
Dd	221039	TTTCTGCACATGCTCTCTCTTTAAGAGGGGTGTGTGCTGGCGGTGATCAACTCTTA	220980
OY	1267	T-----TACGGTATTTGAAAAATAGCACACTTTCAGCTTAGGGCCATATCTA	1317
Dd	220979	TTGAAATGTCGTAATGTAATTAGTACAAATPATCATAGTAATTAAGCTATAGSAAAGC	220920
OY	1318	CTGAGAGTAACTATTCCTGTGCTCTCTAABAAGCCCTAGCTCAAAATCTCTTAAATG	1377
Dd	220919	AAGCTTTTGAGATGTAAAAAAGAACTCTTABAAGCCAAATGACAAATATTTTCAATG	220860
OY	1378	CTGGGTAGCAAGGCTCGTACTTAFTTACAAAGTTGAAAAACAGCCCTCAGAAACAGAT	1437
Dd	220859	CTGCTTTTAAAGATCTTTTATATTTTATCATAAATTTAAACACAAAAAAGGCTTGGGT	220800
OY	1438	TAAATCTCAACAGTAGAGGGTCTATATGATTTAAACAGAGATCTTAAGCCCTGTCA	1497
Dd	220799	TTATGCTTCCAGCTTAAAGGGGTAAATATGATTTAGAGTGGAAATTAATATCTGTCTA	220740
OY	1498	AAGTAAACAGATCAAGCGTTTAAAAATCAGACTTCTGTAGCTAGTCTTATTTTGAACAAG	1557
Dd	220739	AGGTTTACAGAAAGCCGCTTCAAAAATCTCTCTTCAATTCCTGACCTTTTATTAACAACAG	220680
OY	1558	AAGCAATTTTCTCTAATTAACCTAAACAGACCTAGCCGACAGCCAGCAATGCAACAGTA	1617
Dd	220679	AATGTCAATTCACAGATATTTAAAGAAAGAAAAATCTCTGTGTGTGTGTGTATTCCTA	220620
OY	1618	TGGATCCAGAGATG 1631	
Dd	220619	TGGAACCAAGAAATG 220606	